PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/819,669D*

DATE: 10/08/1999
TIME: 13:48:03

INPUT SET: S33581.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

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 1                                    SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5        (i)  APPLICANTS:  Boon-Falleur, Thierry; Van der Bruggen, Thierry;
 6             Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
 7             Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
 8
 9        (ii) TITLE OF INVENTION:  Tumor Rejection Antigen Precursors, Tumor
10             Rejection Antigens and Uses Thereof
11
12        (iii) NUMBER OF SEQUENCES:  26
13
14        (iv) CORRESPONDENCE ADDRESS:
15             (A) ADDRESSEE: Fulbright & Jaworski LLP
16             (B) STREET: 666 Fifth Avenue
17             (C) CITY:  New York City
18             (D) STATE:  New York
19             (E) COUNTRY; USA
20             (F) ZIP:  10103
21
22        (v) COMPUTER READABLE FORM:
23             (A) MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
24             (B) COMPUTER:  IBM
25             (C) OPERATING SYSTEM:  PC-DOS
26             (D) SOFTWARE:  Wordperfect
27
28        (vi) CURRENT APPLICATION DATA:
29             (A) APPLICATION NUMBER:  08/819,669
30             (B) FILING DATE: 17-March-1997
31             (C) CLASSIFICATION:  435
32
33        (vii) PRIOR APPLIATION DATA:
34             (A) APPLICATION NUMBER: 08/142,368
35             (B) FILING DATE: 02-MAY-1994
36
37        (vii) PRIOR APPLICATION DATA:
38             (A) APPLICATION NUMBER: PCT/US92/04354
39             (B) FILING DATE:  22-MAY-1992
40
41        (vii) PRIOR APPLICATION DATA:
42             (A) APPLICATION NUMBER:  07/807,043
43             (B) FILING DATE:  12-DECEMBER-1991
44
45        (vii) PRIOR APPLICATION DATA:
46             (A) APPLICATION NUMBER:  07/764,364
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47                (B) FILING DATE:   23-SEPTEMBER-1991
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49         (vii) PRIOR APPLICATION DATA:
50                (A) APPLICATION NUMBER: 07/728,838
51                (b) FILING DATE:   9-JULY-1991
52
53       . (vii) PRIOR APPLICATION DATA:
54                (A) APPLICATION NUMBER:  07/705,702
55                (B) FILING DATE:   23-May-1991
56
57         (viii) ATTORNEY/AGENT INFORMATION:
58                (A) NAME:  Hanson, Norman D.
59                (B) REGISTRATION NUMBER:  30,946
60                (C) REFERENCE/DOCKET NUMBER:   LUD 5253.5-US
61
62         (ix) TELECOMMUNICATION INFORMATION:
63                (A) TELEPHONE: (212)318-3168
64                (B) TELEFAX: (212)752-5958
65
66
67
68    (2) INFORMATION FOR SEQ ID NO: 1:
69         (i) SEQUENCE CHARACTERISTICS:
70                (A) LENGTH:   462 base pairs
71                (B) TYPE:  nucleic acid
72                (C) STRANDEDNESS: single
73                (D) TOPOLOGY:  linear
74         (ii) MOLECULE TYPE:  genomic DNA
75         (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 1:
76
77
78
79
80    ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG        60
81    ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT       120
82    CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG       180
83    CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC       240
84    CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT       300
85    AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG CATGCATTGT       360
86    GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT       420
87    TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC                         462
88
89
90
91
92    (2) INFORMATION FOR SEQ ID NO: 2:
93         (i) SEQUENCE CHARACTERISTICS:
94                (A) LENGTH:   675 base pairs
95                (B) TYPE:  nucleic acid
96                (C) STRANDEDNESS: single
97                (D) TOPOLOGY:  linear
98         (ii) MOLECULE TYPE:  genomic DNA
99         (xi) SEQUENCE DESCRIPTION:   SEQ ID NO: 2:
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103    Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
104                      5                  10                      15
105    GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA        96
106    Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
107                      20                 25                      30
108    GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA       144
109    Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
110                      35                 40                      45
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112    Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
113                  50                 55                 60
114    TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC       240
115    Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
116    65                     70                 75                     80
117    TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC       288
118    Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
119                      85                 90                      95
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121    Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
122                  100                105                110
123    GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG       384
124    Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
125                  115                120                125
126    GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG       432
127    Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
128              130                135                140
129    GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG       480
130    Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
131    145                    150                155                    160
132    AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC       528
133    Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
134                      165                170                175
135    CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT       576
136    Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
137                      180                185                190
138    GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG       624
139    Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu
140              195                200                210
141    GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT       672
142    Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
143    220                    225                230                235
144
145    TAG                                                                  675
146
147
148
149    (2)  INFORMATION FOR SEQ ID NO: 3:
150         (i)  SEQUENCE CHARACTERISTICS:
151              (A)  LENGTH:   228 base pairs
152              (B)  TYPE:   nucleic acid
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/819,669D*

INPUT SET: S33581.raw

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153          (C) STRANDEDNESS: single
154          (D) TOPOLOGY:  linear
155      (ii) MOLECULE TYPE:  genomic DNA .
156      (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 3:
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158
159
160  GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT        60
161  TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT       120
162  TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACTTT CATATGATAC       180
163  ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTTGAC TTGCATAC                   228
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165
166  (2) INFORMATION FOR SEQ ID NO: 4:
167      (i) SEQUENCE CHARACTERISTICS:
168          (A) LENGTH:  1365 base pairs
169          (B) TYPE:  nucleic acid
170          (C) STRANDEDNESS: single
171          (D) TOPOLOGY:  linear
172      (ii) MOLECULE TYPE:  genomic DNA
173      (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 4:
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180  CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA        250
181  CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT        300
182  AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG        350
183  CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG        400
184  CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT        450
185  ACCCTTTGTG CC                                                462
186  ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA       504
187  GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG       546
188  TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC       588
189  TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC       630
190  ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC       672
191  TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG       714
192  GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC       756
193  GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT       798
194  GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA       840
195  GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA       882
196  GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT       924
197  GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT       966
198  TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG      1008
199  AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT      1050
200  GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG GAG GAG      1092
201  GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT      1134
202  TAG                                                         1137
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211  (2)  INFORMATION FOR SEQ ID NO: 5:
212       (i)  SEQUENCE CHARACTERISTICS:
213            (A)  LENGTH:   4698 base pairs
214            (B)  TYPE:  nucleic acid
215            (C)  STRANDEDNESS: single
216            (D)  TOPOLOGY:   linear
217       (ii)  MOLECULE TYPE:  genomic DNA
218       (xi)  SEQUENCE DESCRIPTION:   SEQ ID NO: 5:
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224  CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA         250
225  CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT         300
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229  ACCCTTTGTG CC                                                  462
230  ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA        504
231  GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG        546
232  TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC        588
233  TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC        630
234  ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC        672
235  TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG        714
236  GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC        756
237  GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT        798
238  GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA        840
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240  GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T                 916
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242  CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC        1016
243  TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC        1066
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/819,669D*

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398   (2) INFORMATION FOR SEQ ID NO: 8:
399       (i) SEQUENCE CHARACTERISTICS:
400           (A) LENGTH:   5674 base pairs
401           (B) TYPE:   nucleic acid
402           (C) STRANDEDNESS: single
403           (D) TOPOLOGY:   linear
404       (ii) MOLECULE TYPE:  genomic DNA
405       (ix) FEATURE:
406           (A) NAME/KEY:   MAGE-1 gene
407       (xi) SEQUENCE DESCRIPTION:   SEQ ID NO:  8:
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409
410   CCCGGGGCAC CACTGGCATC CCTCCCCCTA CCACCCCCAA TCCCTCCCTT        50
411   TACGCCACCC ATCCAAACAT CTTCACGCTC ACCCCAGCC  CAAGCCAGGC       100
412   AGAATCCGGT TCCACCCCTG CTCTCAACCC AGGGAAGCCC AGGTGCCCAG       150
413   ATGTGACGCC ACTGACTTGA GCATTAGTGG TTAGAGAGAA GCGAGGTTTT       200
414   CGGTCTGAGG GGCGGCTTGA GATCGGTGGA GGGAAGCGGG CCCAGCTCTG       250
415   TAAGGAGGCA AGGTGACATG CTGAGGGAGG ACTGAGGACC CACTTACCCC       300
416   AGATAGAGGA CCCCAAATAA TCCCTTCATG CCAGTCCTGG ACCATCTGGT       350
417   GGTGGACTTC TCAGGCTGGG CCACCCCCAG CCCCCTTGCT GCTTAAACCA       400
418   CTGGGGACTC GAAGTCAGAG CTCCGTGTGA TCAGGGAAGG GCTGCTTAGG       450
419   AGAGGGCAGC GTCCAGGCTC TGCCAGACAT CATGCTCAGG ATTCTCAAGG       500
420   AGGGCTGAGG GTCCCTAAGA CCCCACTCCC GTGACCCAAC CCCCACTCCA       550
421   ATGCTCACTC CCGTGACCCA ACCCCCTCTT CATTGTCATT CCAACCCCCA       600
422   CCCCACATCC CCCACCCCAT CCCTCAACCC TGATGCCCAT CCGCCCAGCC       650
423   ATTCCACCCT CACCCCCACC CCCACCCCCA CGCCCACTCC CACCCCCACC       700
424   CAGGCAGGAT CCGGTTCCCG CCAGGAAACA TCCGGGTGCC CGGATGTGAC       750
425   GCCACTGACT TGCGCATTGT GGGGCAGAGA GAAGCGAGGT TTCCATTCTG       800
426   AGGGACGGCG TAGAGTTCGG CCGAAGGAAC CTGACCCAGG CTCTGTGAGG       850
427   AGGCAAGGTG AGAGGCTGAG GGAGGACTGA GGACCCCGCC ACTCCAAATA       900
428   GAGAGCCCCA AATATTCCAG CCCCGCCCTT GCTGCCAGCC CTGGCCCACC       950
429   CGCGGGAAGA CGTCTCAGCC TGGGCTGCCC CCAGACCCCT GCTCCAAAAG      1000
430   CCTTGAGAGA CACCAGGTTC TTCTCCCCAA GCTCTGGAAT CAGAGGTTGC      1050
431   TGTGACCAGG GCAGGACTGG TTAGGAGAGG GCAGGGCACA GGCTCTGCCA      1100
432   GGCATCAAGA TCAGCACCCA AGAGGGAGGG CTGTGGGCCC CCAAGACTGC      1150
433   ACTCCAATCC CCACTCCCAC CCCATTCGCA TTCCCATTCC CCACCCAACC      1200
434   CCCATCTCCT CAGCTACACC TCCACCCCCA TCCCTACTCC TACTCCGTCA      1250
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436   TCACCCTCAC TGCCCCCAAC CCCACCCTCA TCTCTCTCAT GTGCCCCACT      1350
437   CCCATCGCCT CCCCCATTCT GGCAGAATCC GGTTTGCCCC TGCTCTCAAC      1400
438   CCAGGGAAGC CCTGGTAGGC CCGATGTGAA ACCACTGACT TGAACCTCAC      1450
439   AGATCTGAGA GAAGCCAGGT TCATTTAATG GTTCTGAGGG GCGGCTTGAG      1500
440   ATCCACTGAG GGGAGTGGTT TTAGGCTCTG .TGAGGAGGCA AGGTGAGATG      1550
441   CTGAGGGAGG ACTGAGGAGG CACACACCCC AGGTAGATGG CCCCAAAATG      1600
442   ATCCAGTACC ACCCCTGCTG CCAGCCCTGG ACCACCCGGC CAGGACAGAT      1650
443   GTCTCAGCTG GACCACCCCC CGTCCCGTCC CACTGCCACT TAACCCACAG      1700
444   GGCAATCTGT AGTCATAGCT TATGTGACCG GGGCAGGGTT GGTCAGGAGA      1750
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446   ACCCTGGGAG GGAACTGAGG GTTCCCCACC CACACCTGTC TCCTCATCTC        1850
447   CACCGCCACC CCACTCACAT TCCCATACCT ACCCCCTACC CCCAACCTCA        1900
448   TCTTGTCAGA ATCCCTGCTG TCAACCCACG GAAGCCACGG GAATGGCGGC        1950
449   CAGGCACTCG GATCTTGACG TCCCCATCCA GGGTCTGATG GAGGGAAGGG        2000
450   GCTTGAACAG GGCCTCAGGG GAGCAGAGGG AGGGCCCTAC TGCGAGATGA        2050
451   GGGAGGCCTC AGAGGACCCA GCACCCTAGG ACACCGCACC CCTGTCTGAG        2100
452   ACTGAGGCTG CCACTTCTGG CCTCAAGAAT CAGAACGATG GGGACTCAGA        2150
453   TTGCATGGGG GTGGGACCCA GGCCTGCAAG GCTTACGCGG AGGAAGAGGA        2200
454   GGGAGGACTC AGGGGACCTT GGAATCCAGA TCAGTGTGGA CCTCGGCCCT        2250
455   GAGAGGTCCA GGGCACGGTG GCCACATATG GCCCATATTT CCTGCATCTT        2300
456   TGAGGTGACA GGACAGAGCT GTGGTCTGAG AAGTGGGGCC TCAGGTCAAC        2350
457   AGAGGGAGGA GTTCCAGGAT CCATATGGCC CAAGATGTGC CCCCTTCATG        2400
458   AGGACTGGGG ATATCCCCGG CTCAGAAAGA AGGGACTCCA CACAGTCTGG        2450
459   CTGTCCCCTT TTAGTAGCTC TAGGGGGACC AGATCAGGGA TGGCGGTATG        2500
460   TTCCATTCTC ACTTGTACCA CAGGCAGGAA GTTGGGGGGC CCTCAGGGAG        2550
461   ATGGGGTCTT GGGGTAAAGG GGGGATGTCT ACTCATGTCA GGGAATTGGG        2600
462   GGTTGAGGAA GCACAGGCGC TGGCAGGAAT AAAGATGAGT GAGACAGACA        2650
463   AGGCTATTGG AATCCACACC CCAGAACCAA AGGGGTCAGC CCTGGACACC        2700
464   TCACCCAGGA TGTGGCTTCT TTTTCACTCC TGTTTCCAGA TCTGGGGCAG        2750
465   GTGAGGACCT CATTCTCAGA GGGTGACTCA GGTCAACGTA GGGACCCCCA        2800
466   TCTGGTCTAA AGACAGAGCG GTCCCAGGAT CTGCCATGCG TTCGGGTGAG        2850
467   GAACATGAGG GAGGACTGAG GGTACCCCAG GACCAGAACA CTGAGGGAGA        2900
468   CTGCACAGAA ATCAGCCCTG CCCCTGCTGT CACCCCAGAG AGCATGGGCT        2950
469   GGGCCGTCTG CCGAGGTCCT TCCGTTATCC TGGGATCATT GATGTCAGGG        3000
470   ACGGGGAGGC CTTGGTCTGA GAAGGCTGCG CTCAGGTCAG TAGAGGGAGC        3050
471   GTCCCAGGCC CTGCCAGGAG TCAAGGTGAG GACCAAGCGG GCACCTCACC        3100
472   CAGGACACAT TAATTCCAAT GAATTTTGAT ATCTCTTGCT GCCCTTCCCC        3150
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474   TCCTTATCAT GGATGTGAAC TCTTGATTTG GATTTCTCAG ACCAGCAAAA        3250
475   GGGCAGGATC CAGGCCCTGC CAGGAAAAAT ATAAGGGCCC TGCGTGAGAA        3300
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483   CTCACTTCCT CCTTCAGGTT TTCAGGGGAC AGGCCAACCC AGAGGACAGG        3700
484   ATTCCCTGGA GGCCACAGAG GAGCACCAAG GAGAAGATCT GTAAGTAGGC        3750
485   CTTTGTTAGA GTCTCCAAGG TTCAGTTCTC AGCTGAGGCC TCTCACACAC        3800
486   TCCCTCTCTC CCCAGGCCTG TGGGTCTTCA TTGCCCAGCT CCTGCCCACA        3850
487   CTCCTGCCTG CTGCCCTGAC GAGAGTCATC                              3880
488   ATG TCT CTT GAG CAG AGG AGT CTG CAC TGC AAG CCT GAG GAA        3922
489   GCC CTT GAG GCC CAA CAA GAG GCC CTG GGC CTG GTG TGT GTG        3964
490   CAG GCT GCC ACC TCC TCC TCC TCT CCT CTG GTC CTG GGC ACC        4006
491   CTG GAG GAG GTG CCC ACT GCT GGG TCA ACA GAT CCT CCC CAG        4048
492   AGT CCT CAG GGA GCC TCC GCC TTT CCC ACT ACC ATC AAC TTC        4090
493   ACT CGA CAG AGG CAA CCC AGT GAG GGT TCC AGC AGC CGT GAA        4132
494   GAG GAG GGG CCA AGC ACC TCT TGT ATC CTG GAG TCC TTG TTC        4174
495   CGA GCA GTA ATC ACT AAG AAG GTG GCT GAT TTG GTT GGT TTT        4216
496   CTG CTC CTC AAA TAT CGA GCC AGG GAG CCA GTC ACA AAG GCA        4258
497   GAA ATG CTG GAG AGT GTC ATC AAA AAT TAC AAG CAC TGT TTT        4300
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INPUT SET: S33581.raw

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498    CCT GAG ATC TTC GGC AAA GCC TCT GAG TCC TTG CAG CTG GTC        4342
499    TTT GGC ATT GAC GTG AAG GAA GCA GAC CCC ACC GGC CAC TCC        4384
500    TAT GTC CTT GTC ACC TGC CTA GGT CTC TCC TAT GAT GGC CTG        4426
501    CTG GGT GAT AAT CAG ATC ATG CCC AAG ACA GGC TTC CTG ATA        4468
502    ATT GTC CTG GTC ATG ATT GCA ATG GAG GGC GGC CAT GCT CCT        4510
503    GAG GAG GAA ATC TGG GAG GAG CTG AGT GTG ATG GAG GTG TAT        4552
504    GAT GGG AGG GAG CAC AGT GCC TAT GGG GAG CCC AGG AAG CTG        4594
505    CTC ACC CAA GAT TTG GTG CAG GAA AAG TAC CTG GAG TAC GGC        4636
506    AGG TGC CGG ACA GTG ATC CCG CAC GCT ATG AGT TCC TGT GGG        4678
507    GTC CAA GGG CCC TCG CTG AAA CCA GCT ATG TGA                    4711
508    AAGTCCTTGA GTATGTGATC AAGGTCAGTG CAAGAGTTC                     4750
509    GCTTTTTCTT CCCATCCCTG CGTGAAGCAG CTTTGAGAGA GGAGGAAGAG        4800
510    GGAGTCTGAG CATGAGTTGC AGCCAAGGCC AGTGGGAGGG GGACTGGGCC        4850
511    AGTGCACCTT CCAGGGCCGC GTCCAGCAGC TTCCCCTGCC TCGTGTGACA        4900
512    TGAGGCCCAT TCTTCACTCT GAAGAGAGCG GTCAGTGTTC TCAGTAGTAG        4950
513    GTTTCTGTTC TATTGGGTGA CTTGGAGATT TATCTTTGTT CTCTTTTGGA        5000
514    ATTGTTCAAA TGTTTTTTTT TAAGGGATGG TTGAATGAAC TTCAGCATCC        5050
515    AAGTTTATGA ATGACAGCAG TCACACAGTT CTGTGTATAT AGTTTAAGGG        5100
516    TAAGAGTCTT GTGTTTATT CAGATTGGGA AATCCATTCT ATTTTGTGAA         5150
517    TTGGGATAAT AACAGCAGTG GAATAAGTAC TTAGAAATGT GAAAAATGAG        5200
518    CAGTAAAATA GATGAGATAA AGAACTAAAG AAATTAAGAG ATAGTCAATT        5250
519    CTTGCCTTAT ACCTCAGTCT ATTCTGTAAA ATTTTTAAAG ATATATGCAT        5300
520    ACCTGGATTT CCTTGGCTTC TTTGAGAATG TAAGAGAAAT TAAATCTGAA        5350
521    TAAAGAATTC TTCCTGTTCA CTGGCTCTTT TCTTCTCCAT GCACTGAGCA        5400
522    TCTGCTTTTT GGAAGGCCCT GGGTTAGTAG TGGAGATGCT AAGGTAAGCC        5450
523    AGACTCATAC CCACCCATAG GGTCGTAGAG TCTAGGAGCT GCAGTCACGT        5500
524    AATCGAGGTG GCAAGATGTC CTCTAAAGAT GTAGGGAAAA GTGAGAGAGG        5550
525    GGTGAGGGTG TGGGGCTCCG GGTGAGAGTG GTGGAGTGTC AATGCCCTGA        5600
526    GCTGGGGCAT TTTGGGCTTT GGGAAACTGC AGTTCCTTCT GGGGGAGCTG        5650
527    ATTGTAATGA TCTTGGGTGG ATCC                                     5674
528
529
530
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1003    (2) INFORMATION FOR SEQ ID NO: 17:
1004        (i) SEQUENCE CHARACTERISTICS:
1005            (A) LENGTH:  2305 base pairs
1006            (B) TYPE: nucleic acid
1007            (C) STRANDEDNESS: single
1008            (D) TOPOLOGY:  linear
1009        (ii) MOLECULE TYPE:  genomic DNA
1010        (ix) FEATURE:
1011            (A) NAME/KEY:  MAGE-51 gene
1012        (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 17:
1013
1014
1015

1016    GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG          50
1017    GGGACCATTC ACCCCAAGAG GGTGGAGACC TCACAGATTC CAGCCTACCC         100
1018    TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG         150
1019    GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT         200
1020    TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC         250
1021    TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC         300
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INPUT SET: S33581.raw

1022	GCCCCAGAAC	ATATGGGACT	CCAGAGCACC	TGGCCTCACC	CTCTCTACTG	350
1023	TCAGTCCTGC	AGAATCAGCC	TCTGCTTGCT	TGTGTACCCT	GAGGTGCCCT	400
1024	CTCACTTTTT	CCTTCAGGTT	CTCAGGGGAC	AGGCTGACCA	GGATCACCAG	450
1025	GAAGCTCCAG	AGGATCCCCA	GGAGGCCCTA	GAGGAGCACC	AAAGGAGAAG	500
1026	ATCTGTAAGT	AAGCCTTTGT	TAGAGCCTCC	AAGGTTCAGT	TTTTAGCTGA	550
1027	GGCTTCTCAC	ATGCTCCCTC	TCTCTCCAGG	CCAGTGGGTC	TCCATTGCCC	600
1028	AGCTCCTGCC	CACACTCCTG	CCTGTTGCGG	TGACCAGAGT	CGTC	644
1029	ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA					686
1030	GGC CTT GAC ACC CAA GAA GAG CCC TGG GCC TGG TGG GTG TGC					728
1031	AGG CTG CCA CTA CTG AGG AGC AGG AGG CTG TGT CCT CCT CCT					770
1032	CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG					812
1033	GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA					854
1034	TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA					896
1035	AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC					938
1036	CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG					980
1037	TGG CTG ACT TGA					992
1038	TTCATTTTCT	GCTCCTCAAG	TATTAAGTCA	AGGAGCCGGT	CACAAAGGCA	1042
1039	GAAATGCTGG	AGAGCGTCAT	CAAAAATTAC	AAGCGCTGCT	TTCCTGAGAT	1092
1040	CTTCGGCAAA	GCCTCCGAGT	CCTTGCAGCT	GGTCTTTGGC	ATTGACGTGA	1142
1041	AGGAAGCGGA	CCCCACCAGC	AACACCTACA	CCCTTGTCAC	CTGCCTGGGA	1192
1042	CTCCTATGAT	GGCCTGGTGG	TTTAATCAGA	TCATGCCCAA	GACGGGCCTC	1242
1043	CTGATAATCG	TCTTGGGCAT	GATTGCAATG	GAGGGCAAAT	GCGTCCCTGA	1292
1044	CCACAAAATC	TGGGAGGAGC	TGGGTGTGAT	GAAGGTGTAT	GTTGGGAGGG	1342
1045	AGCACAGTGT	CTGTGGGGAG	CCCAGGAAGC	TGCTCACCCA	AGATTGGTG	1392
1046	CAGGAAAACT	ACCTGGAGTA	CCGCAGGTGC	CCAGCAGTGA	TCCCATATGC	1442
1047	TATGAGTTAC	TGTGGGGTCC	AAGGGCACTC	GCTGCTTGAA	AGTACTGGAG	1492
1048	CACGTGGTCA	GGGTCAATGC	AAGAGTTCTC	ATTTCCTACC	CATCCCTGCA	1542
1049	TGAAGCAGCT	TTGAGAGAGG	AGGAAGAGGG	AGTCTGAGCA	TGAGCTGCAG	1592
1050	CCAGGGCCAC	TGCGAGGGGG	GCTGGGCCAG	TGCACCTTCC	AGGGCTCCGT	1642
1051	CCAGTAGTTT	CCCCTGCCTT	AATGTGACAT	GAGGCCCATT	CTTCTCTCTT	1692
1052	TGAAGAGAGC	AGTCAACATT	CTTAGTAGTG	GGTTTCTGTT	CTATTGGATG	1742
1053	ACTTTGAGAT	TTGTCTTTGT	TTCCTTTTGG	AATTGTTCAA	ATGTTCCTTT	1792
1054	TAATGGGTGG	TTGAATGAAC	TTCAGCATTC	AAATTTATGA	ATGACAGTAG	1842
1055	TCACACATAG	TGCTGTTTAT	ATAGTTTAGG	AGTAAGAGTC	TTGTTTTTTA	1892
1056	TTCAGATTGG	GAAATCCATT	CCATTTTGTG	AATTGGGACA	TAGTTACAGC	1942
1057	AGTGGAATAA	GTATTCATTT	AGAAATGTGA	ATGAGCAGTA	AAACTGATGA	1992
1058	GATAAAGAAA	TTAAAAGATA	TTTAATTCTT	GCCTTATACT	CAGTCTATTC	2042
1059	GGTAAAATTT	TTTTTTAAAA	ATGTGCATAC	CTGGATTTCC	TTGGCTTCTT	2092
1060	TGAGAATGTA	AGACAAATTA	AATCTGAATA	AATCATTCTC	CCTGTTCACT	2142
1061	GGCTCATTTA	TTCTCTATGC	ACTGAGCATT	TGCTCTGTGG	AAGGCCCTGG	2192
1062	GTTAATAGTG	GAGATGCTAA	GGTAAGCCAG	ACTCACCCCT	ACCCACAGGG	2242
1063	TAGTAAAGTC	TAGGAGCAGC	AGTCATATAA	TTAAGGTGGA	GAGATGCCCT	2292
1064	CTAAGATGTA	GAG				2305
1065						
1066						
1067						
1068						

1328	(2) INFORMATION FOR SEQ ID NO: 24:
1329	(i) SEQUENCE CHARACTERISTICS:
1330	(A) LENGTH: 2150 base pairs
1331	(B) TYPE: nucleic acid
1332	(C) STRANDEDNESS: single

INPUT SET: S33581.raw

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1333                (D) TOPOLOGY:   linear
1334          (ii) MOLECULE TYPE:  genomic DNA
1335          (ix) FEATURE:
1336                (A) NAME/KEY:   smage-I
1337          (xi) SEQUENCE DESCRIPTION:   SEQ ID NO: 24:
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1339
1340
1341     TCTGTCTGCA TATGCCTCCA CTTGTGTGTA GCAGTCTCAA ATGGATCTCT        50
1342     CTCTACAGAC CTCTGTCTGT GTCTGGCACC CTAAGTGGCT TTGCATGGGC       100
1343     ACAGGTTTCT GCCCCTGCAT GGAGCTTAAA TAGATCTTTC TCCACAGGCC       150
1344     TATACCCCTG CATTGTAAGT TTAAGTGGCT TTATGTGGAT ACAGGTCTCT       200
1345     GCCCTTGTAT GCAGGCCTAA GTTTTTCTGT CTGCTTAACC CCTCCAAGTG       250
1346     AAGCTAGTGA AAGATCTAAC CCACTTTTGG AAGTCTGAAA CTAGACTTTT       300
1347     ATGCAGTGGC CTAACAAGTT TTAATTTCTT CCACAGGGTT TGCAGAAAAG       350
1348     AGCTTGATCC ACGAGTTCAG AAGTCCTGGT ATGTTCCTAG AAAG            394
1349     ATG TTC TCC TGG AAA GCT TCA AAA GCC AGG TCT CCA TTA AGT       436
1350     CCA AGG TAT TCT CTA CCT GGT AGT ACA GAG GTA CTT ACA GGT       478
1351     TGT CAT TCT TAT CCT TCC AGA TTC CTG TCT GCC AGC TCT TTT       520
1352     ACT TCA GCC CTG AGC ACA GTC AAC ATG CCT AGG GGT CAA AAG       562
1353     AGT AAG ACC CGC TCC CGT GCA AAA CGA CAG CAG TCA CGC AGG       604
1354     GAG GTT CCA GTA GTT CAG CCC ACT GCA GAG GAA GCA GGG TCT       646
1355     TCT CCT GTT GAC CAG AGT GCT GGG TCC AGC TTC CCT GGT GGT       688
1356     TCT GCT CCT CAG GGT GTG AAA ACC CCT GGA TCT TTT GGT GCA       730
1357     GGT GTA TCC TGC ACA GGC TCT GGT ATA GGT GGT AGA AAT GCT       772
1358     GCT GTC CTG CCT GAT ACA AAA AGT TCA GAT GGC ACC CAG GCA       814
1359     GGG ACT TCC ATT CAG CAC ACA CTG AAA GAT CCT ATC ATG AGG       856
1360     AAG GCT AGT GTG CTG ATA GAA TTC CTG CTA GAT AAA TTT AAG       898
1361     ATG AAA GAA GCA GTT ACA AGG AGT GAA ATG CTG GCA GTA GTT       940
1362     AAC AAG AAG TAT AAG GAG CAA TTC CCT GAG ATC CTC AGG AGA       982
1363     ACT TCT GCA CGC CTA GAA TTA GTC TTT GGT CTT GAG TTG AAG      1024
1364     GAA ATT GAT CCC AGC ACT CAT CCC TAT TTG CTG GTA GGC AAA      1066
1365     CTG GGT CTT TCC ACT GAG GGA AGT TTG AGT AGT AAC TGG GGG      1108
1366     TTG CCT AGG ACA GGT CTC CTA ATG TCT GTC CTA GGT GTG ATC      1150
1367     TTC ATG AAG GGT AAC CGT GCC ACT GAG CAA GAG GTC TGG CAA      1192
1368     TTT CTG CAT GGA GTG GGG GTA TAT GCT GGG AAG AAG CAC TTG      1234
1369     ATC TTT GGC GAG CCT GAG GAG TTT ATA AGA GAT GTA GTG CGG      1276
1370     GAA AAT TAC CTG GAG TAC CGC CAG GTA CCT GGC AGT GAT CCC      1318
1371     CCA AGC TAT GAG TTC CTG TGG GGA CCC AGA GCC CAT GCT GAA      1360
1372     ACA ACC AAG ATG AAA GTC CTG GAA GTT TTA GCT AAA GTC AAT      1402
1373     GGC ACA GTC CCT AGT GCC TTC CCT AAT CTC TAC CAG TTG GCT      1444
1374     CTT AGA GAT CAG GCA GGA GGG GTG CCA AGA AGG AGA GTT CAA      1486
1375     GGC AAG GGT GTT CAT TCC AAG GCC CCA TCC CAA AAG TCC TCT      1528
1376     AAC ATG TAG                                                 1537
1377     TTGAGTCTGT TCTGTTGTGT TTGAAAAACA GTCAGGCTCC TAATCAGTAG      1587
1378     AGAGTTCATA GCCTACCAGA ACCAACATGC ATCCATTCTT GGCCTGTTAT      1637
1379     ACATTAGTAG AATGGAGGCT ATTTTTGTTA CTTTTCAAAT GTTTGTTTAA      1687
1380     CTAAACAGTG CTTTTTGCCA TGCTTCTTGT TAACTGCATA AAGAGGTAAC      1737
1381     TGTCACTTGT CAGATTAGGA CTTGTTTTGT TATTTGCAAC AAACTGGAAA      1787
1382     ACATTATTTT GTTTTTACTA AAACATTGTG TAACATTGCA TTGGAGAAGG      1837
1383     GATTGTCATG GCAATGTGAT ATCATACAGT GGTGAAACAA CAGTGAAGTG      1887
1384     GGAAAGTTTA TATTGTTAAT TTTGAAAATT TTATGAGTGT GATTGCTGTA      1937
1385     TACTTTTTTC TTTTTTGTAT AATGCTAAGT GAAATAAAGT TGGATTTGAT      1987
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INPUT SET: S33581.raw

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1386   GACTTTACTC AAATTCATTA GAAAGTAAAT CGTAAAACTC TATTACTTTA        2037
1387   TTATTTTCTT CAATTATGAA TTAAGCATTG GTTATCTGGA AGTTTCTCCA        2087
1388   GTAGCACAGG ATCTAGTATG AAATGTATCT AGTATAGGCA CTGACAGTGA        2137
1389   GTTATCAGAG TCT                                                2150
1390
1391
1392
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/819,669D*

INPUT SET: S33581.raw

Line	Error	Original Text
31	Wrong Classification	(C) CLASSIFICATION: 435